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FIG. 1A

## PRMA\_ECOLI

RRMA\_ECOLI  
S. typhimurium  
Yersinia  
V. cholerae  
Pseudo. putida  
P. aeruginosa  
Strep. fradiae  
B. subtilis  
Lacto. lactis  
Strep. pneumoniae

TTT B1 B2 TT B3 TT B4  
1 10 20 30 40 50  
..... NSPSCPLCHQPLSRBK. NSYICPDR. HOPDMAEGYVNLDPVQHNKSRDPGDS  
..... MSFTCPPLCHQPLTQIH. NSVICPDR. HOPDMAEGYVNLDPVQHNKSRDPGDS  
..... NSYOCPLCHQALQLSQ. QQWCCSN. HOPDMAEGYVNLDPVQHNKSRDPGDS  
..... MLIETTMTFCPLCEHPLTLNQ. NTYACINR. HOPDMAEGYVNLDPVQHNKSRDPGDS  
..... MLIACPLCQAPLTLNR. NCVVCPAG. HRPDRAROGYVNLDPVQHNKSRDPGDS  
..... MLIACPLCSAALGVD. NCVACPPAG. HRPDRAROGYVNLDPVQHNKSRDPGDS  
..... MKKNVVRYLRCPHCAAPURSSD. RTLRCENG. HTPGVAROGYVNLDPVQHNKSRDPGDS  
..... MKRTVDFSMRCPDCHDSMDAASCKSLICTERG. HTPGVAROGYVNLDPVQHNKSRDPGDS  
..... NLKKIEKAYLLLEBNVENLRCPDCHCKWPLAA. YALKEENN. HTYMLNKKCYVNLDPVQHNKSRDPGDS  
..... MNTNLKPKLQRFASATAPACPTICENLTLLE. TNPKECNR. HSPDLAKFGYVNLDPVQHNKSRDPGDS

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α1 α2 α3 α4 α5 α6  
60 70 80 90 100 110  
AEMMAARRAFIDAGHTOPURDAVINLRRERLDD.. KATAVLDIGCCGEGYTHAFAADALP... EITTFG  
AEMMAARRAFIDAGHTOPURDAVINLRRERLDD.. SATAILDIGCCGEGYTHAFAEALP... GVTTFG  
PEMMAARRAFIDAGHTOPURDAVINLRRERLDD.. DATRLDIGCCGEGYTHAFAADRLNK. RQMAIFG  
KEMMAARRAFIDAGHTOPURDAVINLRRERLDD.. RQDTLDIGCCGEGYTHAFAALRQDQAQIFG  
QAMVEARRAFIDAGHTOPURDAVINLRRERLDD.. PCAMLDIGCCGEGYTHAFAAALP... AADGTA  
AAMVEARRAFIDAGHTOPURDAVINLRRERLDD.. DRRMLDIGCCGEGYTHAFAAALP... CAEGYA  
.. MVAARRAFIDAGHTOPURDAVINLRRERLDD.. APDCVVDIGCCGEGYTHAFAAALP... DABGLL  
AEMMAARRAFIDAGHTOPURDAVINLRRERLDD.. LSHPKSGHEAPTILDSGCGEASHLNAICGPDYAG. KAAICTG  
RKMPEPARRAFIDAGHTOPURDAVINLRRERLDD.. NLDDVGTGEGSFLLELE... AGAKFA  
KEMMAARRAFIDAGHTOPURDAVINLRRERLDD.. KTTTTLDIGCCGEGYTHAFAAALP... EKTIFYA

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α4 α5 α6 α7 α8 α9  
120 130 140 150 160 170 180  
LDVSKVAIHAARAKRYD.. QVTECVASSSHR. LPPSTISMDALIRIYADCKAEELARVUNPGGVVITATPG  
LDVAKTAIHAARAKRYD.. QVTECVASSSHR. LPPSTISMDALIRIYADCKAEELARVUNPGGVVITATPG  
LDVAKVAIHAARAKRYD.. QVTECVASSSHR. LPPSTISMDALIRIYADCKAEELARVUNPGGVVITATPG  
LDVSKVAIHAARAKRYD.. QVTECVASSSHR. LPPSTISMDALIRIYADCKAEELARVUNPGGVVITATPG  
LDVSKVAIHAARAKRYD.. QVTECVASSSHR. LPPSTISMDALIRIYADCKAEELARVUNPGGVVITATPG  
LDVSKVAIHAARAKRYD.. QVTECVASSSHR. LPPSTISMDALIRIYADCKAEELARVUNPGGVVITATPG  
LDVSKVAIHAARAKRYD.. QVTECVASSSHR. LPPSTISMDALIRIYADCKAEELARVUNPGGVVITATPG  
LDVSKVAIHAARAKRYD.. QVTECVASSSHR. LPPSTISMDALIRIYADCKAEELARVUNPGGVVITATPG  
LDVSKVAIHAARAKRYD.. QVTECVASSSHR. LPPSTISMDALIRIYADCKAEELARVUNPGGVVITATPG  
LDVSKVAIHAARAKRYD.. QVTECVASSSHR. LPPSTISMDALIRIYADCKAEELARVUNPGGVVITATPG

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α6 α7 α8 α9 α10 α11  
190 200 210 220 230 240  
PRHIMELKGLI.. YNEVHLHAP.. HADOLEGFTLOOSAEFCYPMRURGDEHVA.. LLOMTFPANRRAKPEV  
PHHIMELKGLI.. YDEVRLHAP.. YTELDGFTLOOSTRLAYHMLTAEAAVA.. LLOMTFPANRRAKPEV  
PRHIMELKGLI.. YDEVRLHAP.. YTELDGFTLOOSTRLAYHMLTAEAAVA.. LLOMTFPANRRAKPEV  
ARHIMELKGLI.. YDEVRLHAP.. YTELDGFTLOOSTRLAYHMLTAEAAVA.. LLOMTFPANRRAKPEV  
SGHIMELKGLI.. YDEVRLHAP.. YTELDGFTLOOSTRLAYHMLTAEAAVA.. LLOMTFPANRRAKPEV  
SAHIMELKGLI.. YDEVRLHAP.. YTELDGFTLOOSTRLAYHMLTAEAAVA.. LLOMTFPANRRAKPEV  
QDHIMELKGLI.. YDEVRLHAP.. YTELDGFTLOOSTRLAYHMLTAEAAVA.. LLOMTFPANRRAKPEV  
SDYIMELKGLI.. YDEVRLHAP.. YTELDGFTLOOSTRLAYHMLTAEAAVA.. LLOMTFPANRRAKPEV  
RNTIMELKGLI.. YDEVRLHAP.. YTELDGFTLOOSTRLAYHMLTAEAAVA.. LLOMTFPANRRAKPEV  
ENHIMELKGLI.. YDEVRLHAP.. YTELDGFTLOOSTRLAYHMLTAEAAVA.. LLOMTFPANRRAKPEV

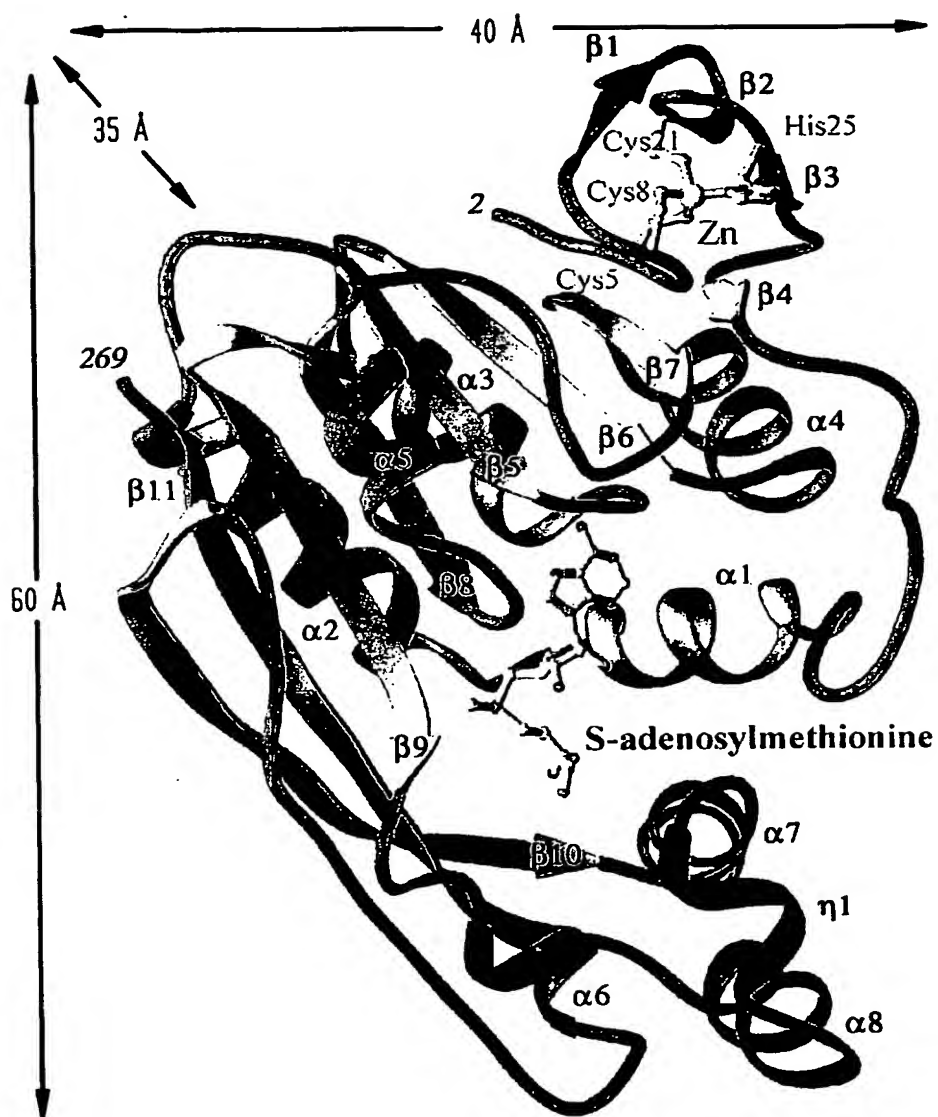
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α8 α9 α10 α11  
250 260 270 280  
WQTLLAKEVFDGOTDFMHLWQRSY.....  
WQTLAKASAGLSGOTDFMHLWQRR.....  
CQTLAKAQSPSCGOTDFMHLWQRR.....  
KHRVSGDSTPEGADDFMHLWQRR.....  
RA.. RVIDQPEPEVTVSMRYDYFVRQD.....  
RA.. RIL.. AEPHEVSVAMRYDHLQRD.....  
LARRIAELPGIHEVTVSMRYDYFVRQD.....  
VSLKREKMSADITVDVHLIGMK.....  
KKFAKRNPPETARIMVQHLIGIK.....  
IDMSK... LTEITIEAGLVLGKAP.....

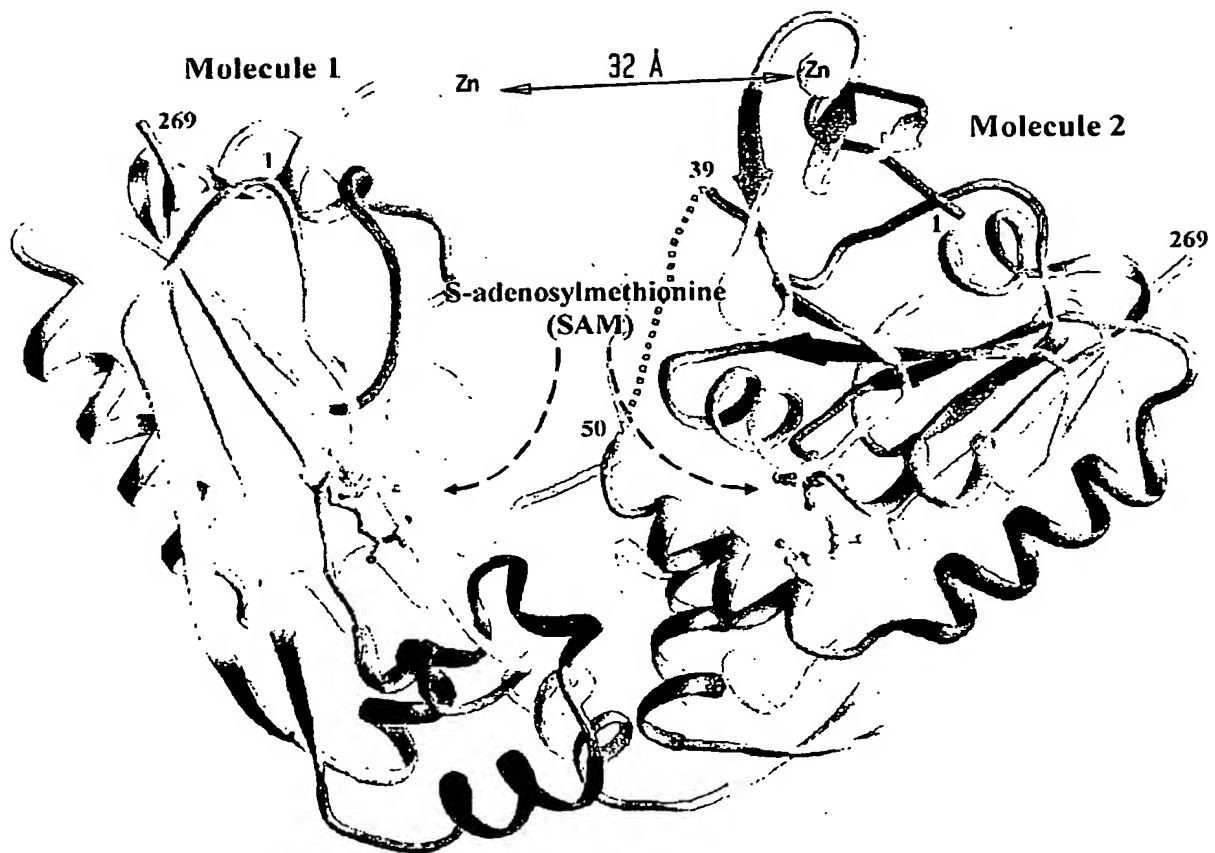
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FIG. 1B



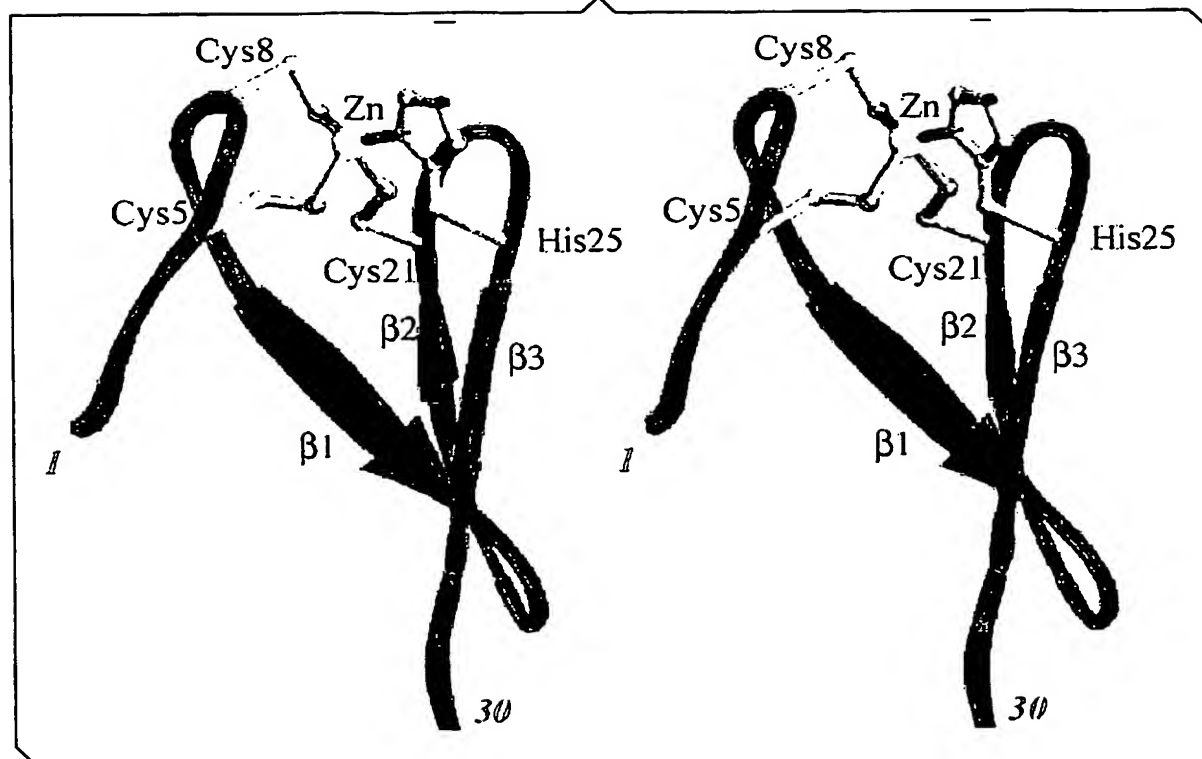
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FIG. 2A



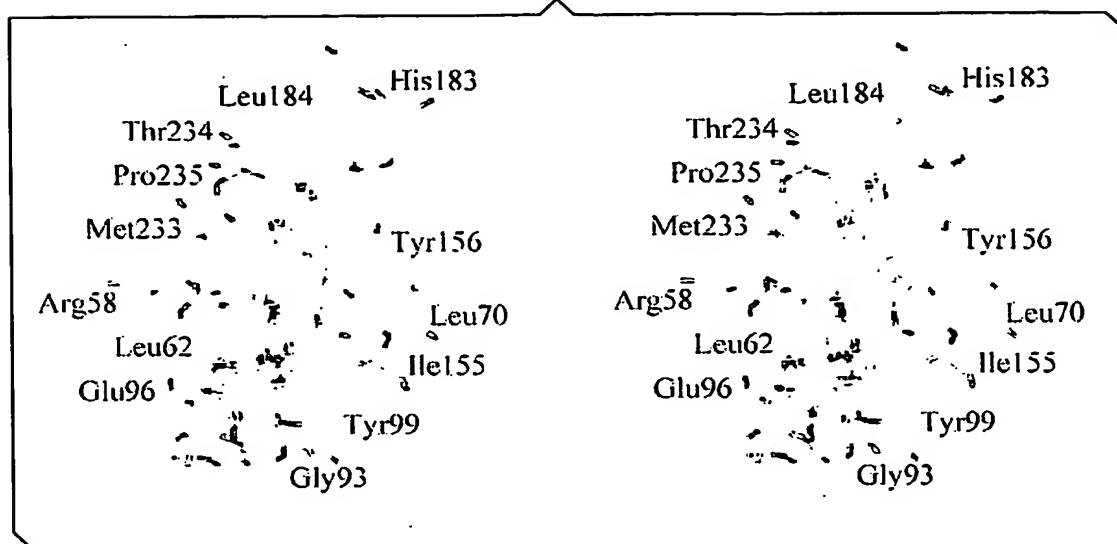
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FIG. 2B



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FIG. 2C



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FIG. 3

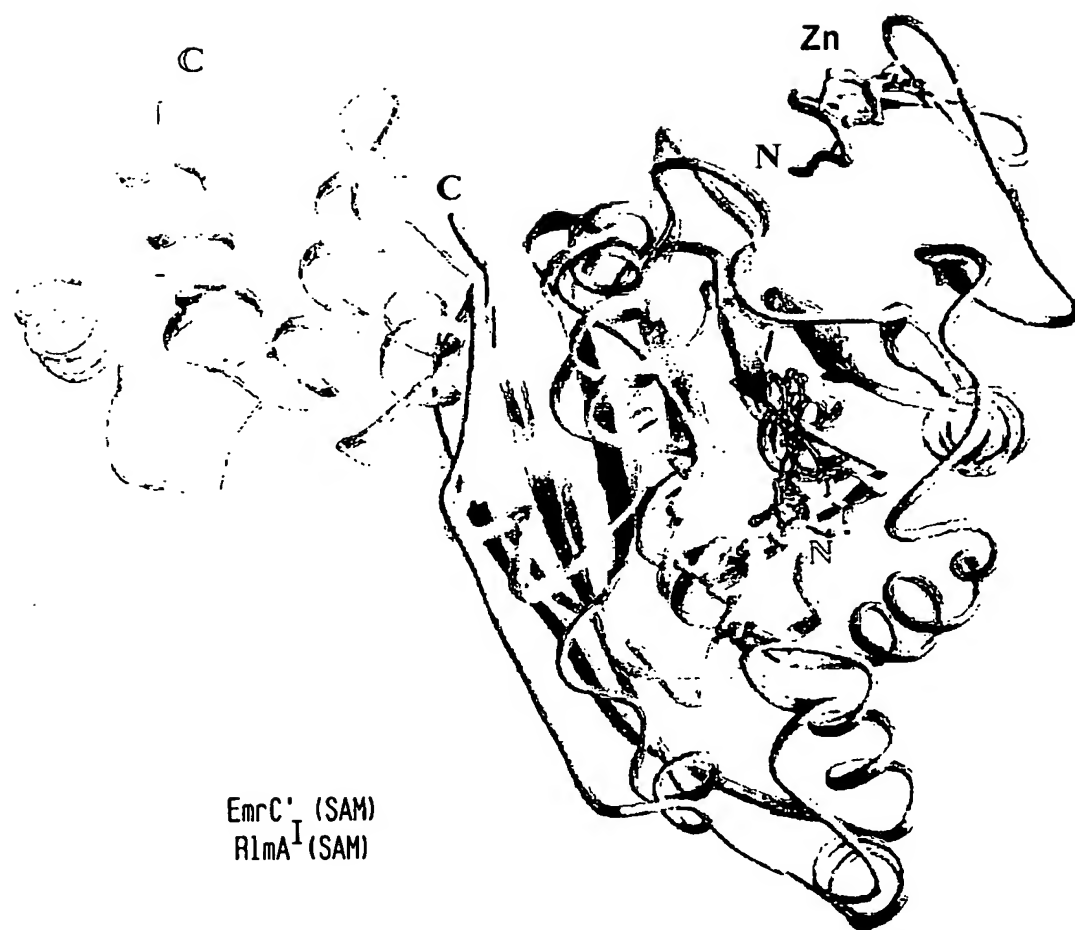


FIG. 4B

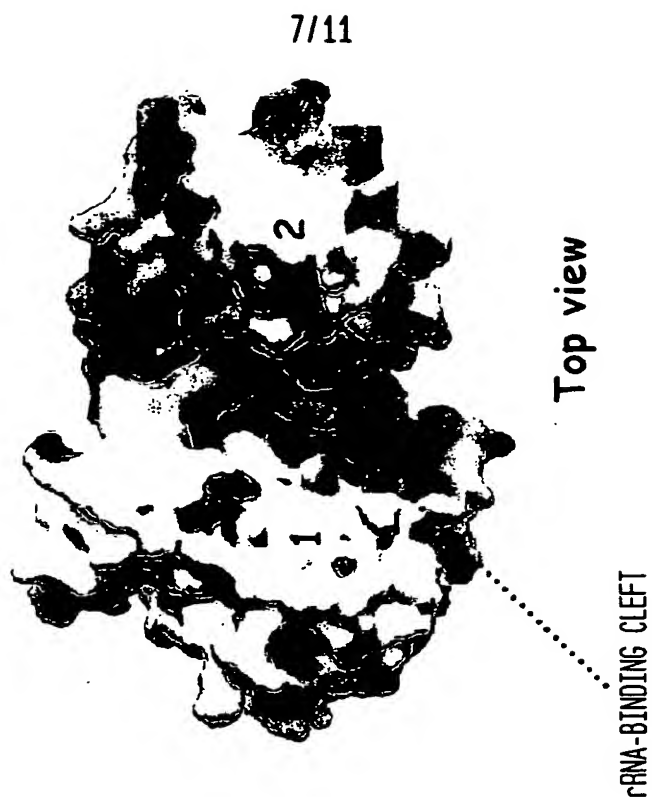
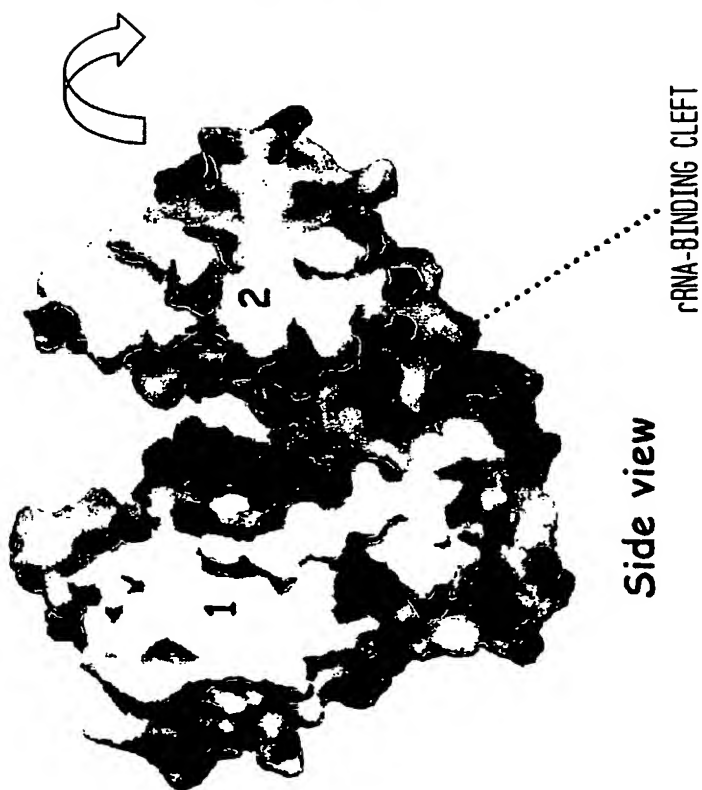
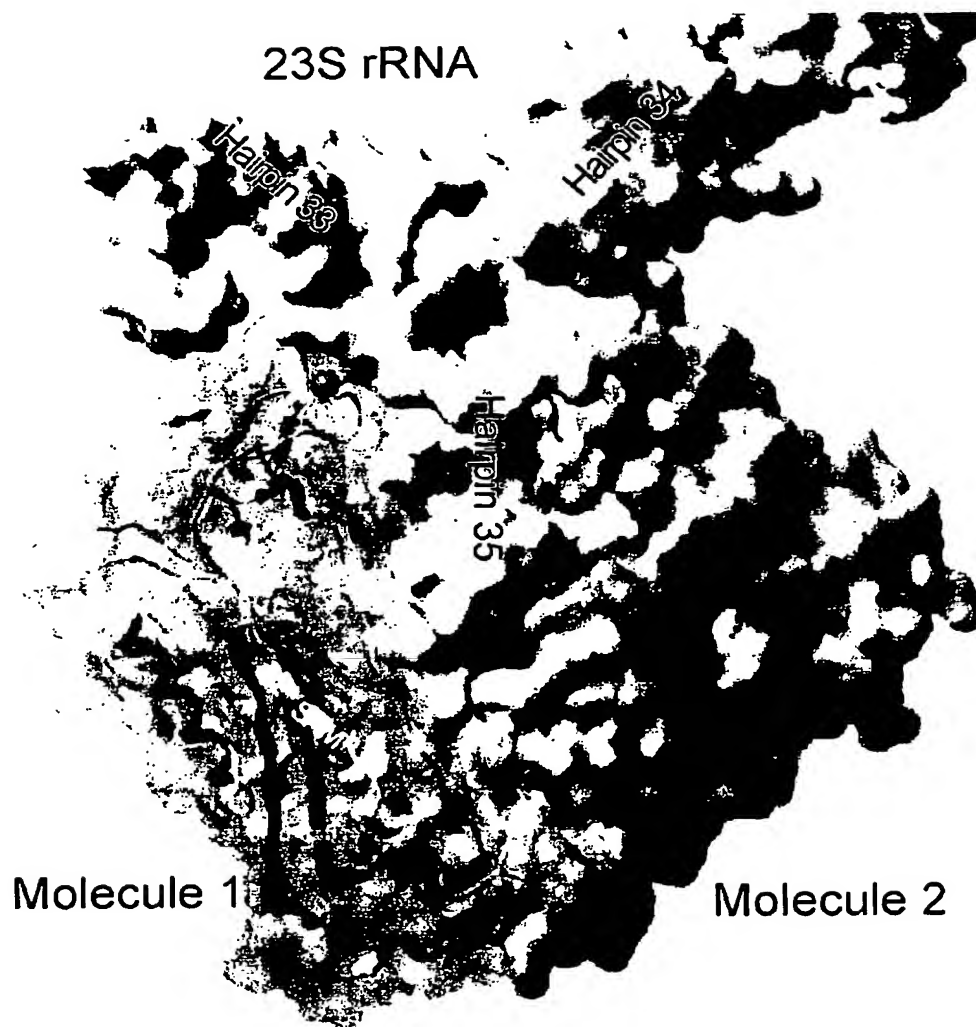


FIG. 4A



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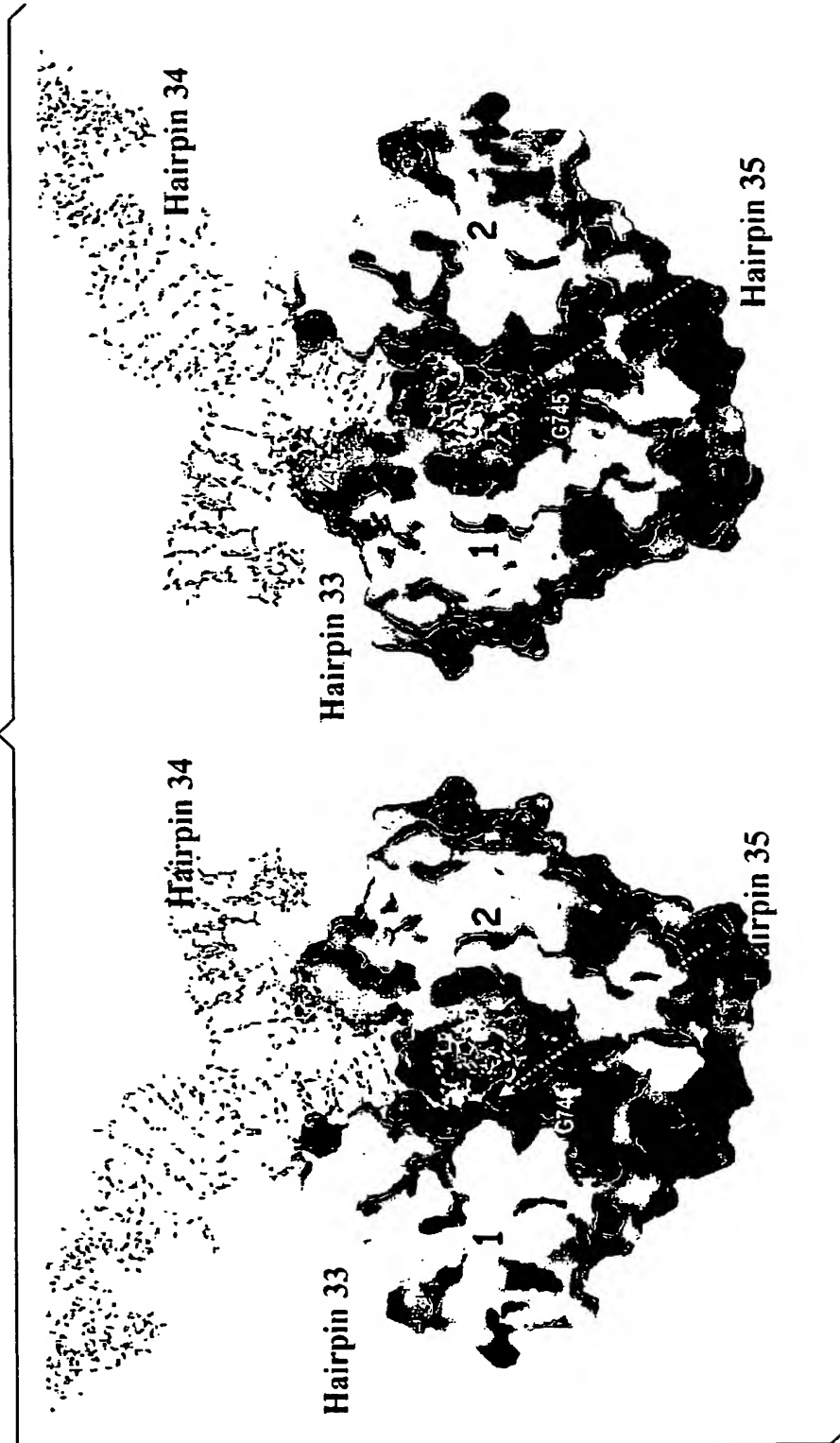
FIG. 5A





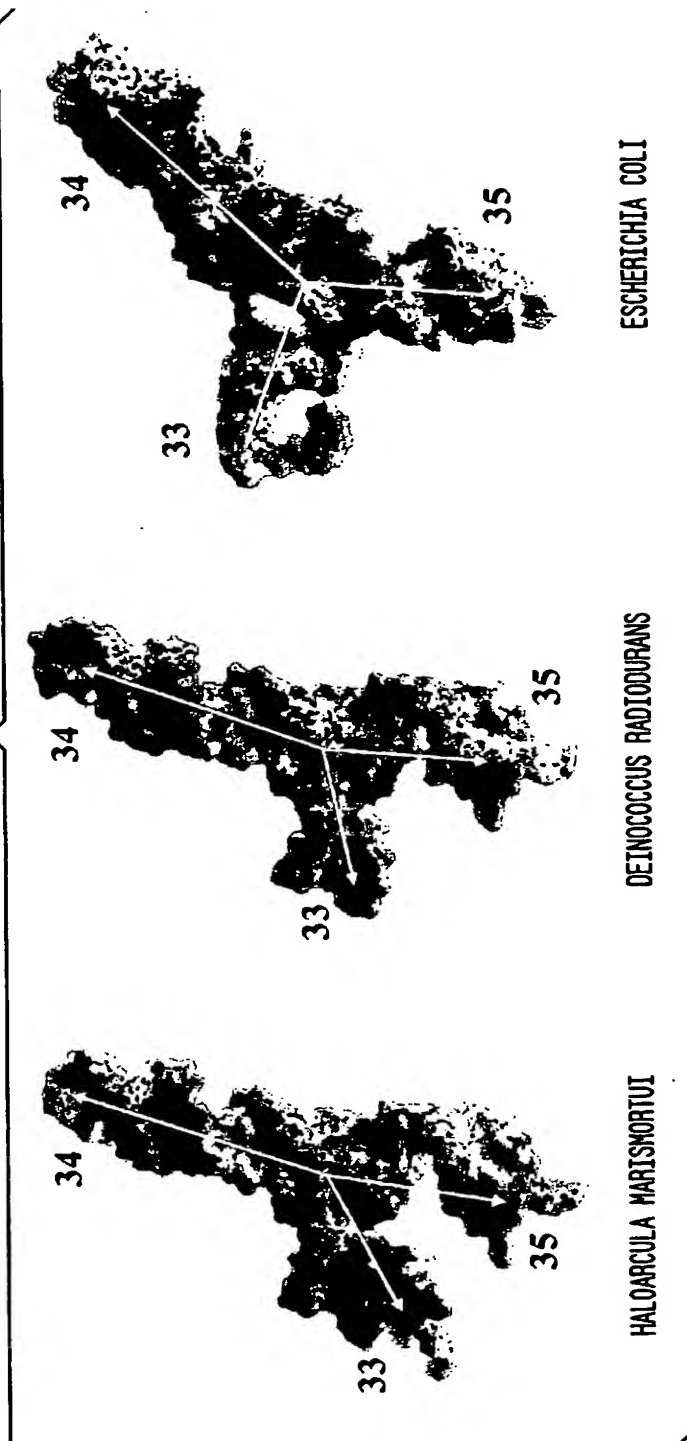
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FIG. 5B



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FIG. 5C



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FIG. 5D

